

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/886,313DATE: 02/11/2000
TIME: 17:10:41

INPUT SET: S34701.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Wright, Jim A.
Young, Aiping H.(ii) TITLE OF INVENTION: INHIBITING NEOPLASTIC CELLS UTILIZING
THE RIBONUCLEOTIDE REDUCTASE UTR

(iii) NUMBER OF SEQUENCES: 50

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Kohn & Associates
(B) STREET: 30500 Northwestern Hwy.
(C) CITY: Farmington Hills
(D) STATE: Michigan
(E) COUNTRY: US
(F) ZIP: 48334

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kohn, Kenneth I.
(B) REGISTRATION NUMBER: 30,955
(C) REFERENCE/DOCKET NUMBER: 0227.00003

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (248) 539-5050
(B) TELEFAX: (248) 539-5055

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 523 base pairs
(B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear
49
50 (ii) MOLECULE TYPE: cDNA
51
52 (iii) HYPOTHETICAL: NO
53
54 (vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Homo sapiens
56
57 (ix) FEATURE:
58 (A) NAME/KEY: 3'UTR
59 (B) LOCATION: 1..523
60
61
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64 GGAAAGACTT GGAAGAGACC AGCATGCTT CAGTAGCCAA ACTACTTCTT GAGCATAGAT 60
65
66 AGGTATAGTG GGTGTGCTTG AGGTGGTAAG GCTTTGCTGG ACCCTGTTGC AGGCAAAAGG 120
67
68 ACTAATTGAT TTAAGTACT GTTAATGATG TTAATGATTT TTTTAAAC TCATATATTG 180
69
70 GGATTTTCAC CAAATAATG CTTTGA AAAAGAAAAA AAAACGGATA TATTGAGAAT 240
71
72 CAAAGTAGAA GTTTAGGAA TGCAAAATAA GTCATCTTGC ATACAGGGAG TGTTAAGTA 300
73
74 AGGTTTCATC ACCCATTAG CATGCTTTTC TGAAGACTTC AGTTTGTTA AGGAGATTTA 360
75
76 GTTTTACTGC TTGACTGGT GGGTCTCTAG AAGCAAACT GAGTGATAAC TCATGAGAAG 420
77
78 TACTGATAGG ACCTTTATCT GGATATGGTC CTATAGGTTA TTCTGAAATA AAGATAAACA 480
79
80 TTTCTAAGTG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 523
81
82 (2) INFORMATION FOR SEQ ID NO:2:
83
84 (i) SEQUENCE CHARACTERISTICS:
85 (A) LENGTH: 1136 base pairs
86 (B) TYPE: nucleic acid
87 (C) STRANDEDNESS: single
88 (D) TOPOLOGY: linear
89
90 (ii) MOLECULE TYPE: cDNA
91
92 (iii) HYPOTHETICAL: NO
93
94 (vi) ORIGINAL SOURCE:
95 (A) ORGANISM: Homo sapiens
96
97 (ix) FEATURE:
98 (A) NAME/KEY: 3'UTR
99 (B) LOCATION: 1..1136

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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100 ATGAACTGAA GATGTGCCCT TACTGGCTG ATTTTTTTT TCCATCTCAT AAGAAAAATC      60
101
102 AGCTGAAAGT TTACCAACTA GCCACACCAT GAATTGTCG TAATGTTTCA TAACAGCATC      120
103
104 TTTAAAAGTG TGTAGCTACC TCACAACCAG TCCTGTCTGT TTATAGTGCT GGTAGTATCA      180
105
106 CCTTTTGCCA GAAGGCCTGG CTGGCTGTGA CTTACCATAG CAGTGACAAT GGCAGTCTTG      240
107
108 GCTTTAAAGT GAGGGGTGAC CCTTTAGTGA GCTTAGCACA GCGGGATTAA ACAGTCCTTT      300
109
110 AACCAGCACA GCCAGTTAAA AGATGCAGCC TCACTGCTTC AACGCAGATT TTAATGTTTA      360
111
112 CTTAAATATA AACCTGGCAC TTTACAAACA AATAACATT GTTTTGTACT CACGGCGGCG      420
113
114 ATAATAGCTT GATTTATTGG GTTCTACAC CAAATACATT CTCCTGACCA CTAATGGGAG      480
115
116 CCAATTCACA ATTCACCTAA TGAATAAGT AAGTTAACT TGTGTAGACT AAGCATGTAA      540
117
118 TTTTAAAGTT TTATTTTAAT GAATTTAAAT ATTTGTTAAC CAACTTTAAA GTCAGTCCTG      600
119
120 TGTATACCTA GATATTAGTC AGTTGGTGCC AGATAGAAGA CAGGTTGTGT TTTTATCCTG      660
121
122 TGGCTTGTGT AGTGCTCTGG GATTCTCTGC CCCCTCTGAG TAGAGTGTTG TGGGATAAAG      720
123
124 GAATCTCTCA GGGCAAGGAG CTTCTTAAAT TAAATCACTA GAAATTTAGG GGTGATCTGG      780
125
126 GCCTTCATAT GTGTGAGAAG CCGTTTCATT TTATTTCTCA CTGTATTTTC CTCACGCTCT      840
127
128 GGTTGATGAG AAAAAATTCT TGAAGAGTTT TCATATGTGG GAGCTAAGGT AGTATTGTAA      900
129
130 AATTTCAGT CATCCTTAAA CAAATGATC CACCTAAGAT CTTGCCCCCTG TTAAGTGGTG      960
131
132 AAATCACTA GAGGTGGTTC CTACAAGTTG TTCATTCTAG TTTTGTGGTG TGTAAGTAGG      1020
133
134 TTGTGTGAGT TAATTCATT ATATTTACTA TGTCTGTTAA ATCAGAAATT TTTTATTATC      1080
135
136 TAGTGTCTTC TAGATTTTAC CTGTAGTTCA TAAAAAATAA AAAAAAATAA AAAAAA      1136
137
138 (2) INFORMATION FOR SEQ ID NO:3:
139
140 (i) SEQUENCE CHARACTERISTICS:
141
142 (A) LENGTH: 20 base pairs
143
144 (B) TYPE: nucleic acid
145
146 (C) STRANDEDNESS: single
147
148 (D) TOPOLOGY: linear
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153
154
155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
156 GGATTAGGT GACACTATAG
157
158 (2) INFORMATION FOR SEQ ID NO:4: 20
159
160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 18 base pairs
162 (B) TYPE: nucleic acid
163 (C) STRANDEDNESS: single
164 (D) TOPOLOGY: linear
165
166
167
168
169
170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
171 TGAGAAAAGC GGGGCCTG
172
173 (2) INFORMATION FOR SEQ ID NO:5: 18
174
175 (i) SEQUENCE CHARACTERISTICS:
176 (A) LENGTH: 21 base pairs
177 (B) TYPE: nucleic acid
178 (C) STRANDEDNESS: single
179 (D) TOPOLOGY: linear
180
181
182
183
184
185
186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
187 TAAGTAACTG ATCGTGTGCT C
188
189 (2) INFORMATION FOR SEQ ID NO:6: 21
190
191 (i) SEQUENCE CHARACTERISTICS:
192 (A) LENGTH: 20 base pairs
193 (B) TYPE: nucleic acid
194 (C) STRANDEDNESS: single
195 (D) TOPOLOGY: linear
196
197
198
199
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201
202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
203 GAGTTTTCAT ATGTGGGAGC
204
205

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206 (2) INFORMATION FOR SEQ ID NO:7:
207
208 (i) SEQUENCE CHARACTERISTICS:
209 (A) LENGTH: 20 base pairs
210 (B) TYPE: nucleic acid
211 (C) STRANDEDNESS: single
212 (D) TOPOLOGY: linear
213
214
215
216
217
218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
219
220 GAGTTTCTC ATATGTGGGA
221
222 (2) INFORMATION FOR SEQ ID NO:8:
223
224 (i) SEQUENCE CHARACTERISTICS:
225 (A) LENGTH: 20 base pairs
226 (B) TYPE: nucleic acid
227 (C) STRANDEDNESS: single
228 (D) TOPOLOGY: linear
229
230
231
232
233
234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
235
236 AATGAACTGA AGATGTGCCG
237
238 (2) INFORMATION FOR SEQ ID NO:9:
239
240 (i) SEQUENCE CHARACTERISTICS:
241 (A) LENGTH: 20 base pairs
242 (B) TYPE: nucleic acid
243 (C) STRANDEDNESS: single
244 (D) TOPOLOGY: linear
245
246
247
248
249
250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
251
252 AGGAATCTCT CAGGCAAGG
253
254 (2) INFORMATION FOR SEQ ID NO:10:
255
256 (i) SEQUENCE CHARACTERISTICS:
257 (A) LENGTH: 20 base pairs
258 (B) TYPE: nucleic acid

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***** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

174 (2) INFORMATION FOR SEQ ID NO:5:
175
176 (i) SEQUENCE CHARACTERISTICS:
177 (A) LENGTH: 21 base pairs
178 (B) TYPE: nucleic acid
179 (C) STRANDEDNESS: single
180 (D) TOPOLOGY: linear
181
182
183
184
185
186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
187
188 TAAGTAACTG ATCGTGTGCT C
189

21

895 (2) INFORMATION FOR SEQ ID NO:50:
896
897 (i) SEQUENCE CHARACTERISTICS:
898 (A) LENGTH: 21 base pairs
899 (B) TYPE: nucleic acid
900 (C) STRANDEDNESS: single
901 (D) TOPOLOGY: linear
902
903
904
905
906
907 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
908
909 TTAAGACTTT TTACGCGATT C
910

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/886,313*

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INPUT SET: S34701.raw

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Original Text